SEQUENCE LISTING

<110> Weinmann, Roberto
Einspahr, Howard M.
Krystek, Jr., Stanley R.
Sack, John A.
Salvati, Mark E.
Tokarski, John S.
Attar, Ricardo M.
Wang, Chihuei

<120> Crystallographic Structure of the Androgen Receptor Ligand Binding Domain

<130> BMS-0010

<140><141>

<150> 60/159,394

<151> 1999-10-14

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 260

<212> PRT

<213> Rattus sp.

<400> 1

Gly Ser His Met Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn 1 5 10 15

Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn 20 25 30

Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu 35 40 45

Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro 50 55 60

Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr 65 70 75 80

Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr

Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn 100 105 110

Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met 115 120 125

Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu 130 135 140

Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp 145 150 155 160

Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile 165 170 175

Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser 180 185 190

Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln 195 200 205

Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys 210 215 220

Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile 225 230 235 240

Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr 245 250 255

Phe His Thr Gln 260

<210> 2

<211> 255

<212> PRT

<213> Rattus sp.

<400> 2

Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser 1 5 10 15

Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp 20 25 30



Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln
35 40 45

Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn 50 55 60

Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser 65 70 75 80

Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly 85 90 95

Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Arg Met 100 105 110

Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr Met Trp Gln Ile Pro 115 120 125

Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu Glu Phe Leu Cys Met 130 135 140

Lys Val Leu Leu Leu Leu Asn Thr Ile Pro Leu Glu Gly Leu Arg Ser 145 150 155 160

Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr Ile Arg Glu Leu Ile 165 170 175

Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val Ser Ser Ser Gln Arg 180 185 190

Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu His Asp Leu Val Lys 195 200 205

Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile Gln Ser Arg Ala Leu 210 215 220

Ser Val Glu Phe Pro Glu Met Met Ser Glu Val Ile Ala Ala Gln Leu 225 230 235 240

Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu Leu Phe His Lys 245 250 255

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>		
<223> Description of Artificial Sequence:	Synthetic	
<400> 3		
catatgattg aaggctatga atgtcaacct atcttt		36
<210> 4		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:	Synthetic	
<400> 4		
tcactgtgtg tggaaataga tggg		24